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0911

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/943,002

DATE: 09/18/2001
TIME: 15:51:22

Input Set : A:\78973-1C seq 28-08-01 v1.txt
Output Set: N:\CRF3\09182001\I943002.raw

3 <110> APPLICANT: Duncan, Roy
 5 <120> TITLE OF INVENTION: NOVEL REOVIRUS-DERIVED PROTEINS AND USES THEREFOR
 7 <130> FILE REFERENCE: 78973-1C
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/943,002
 C--> 10 <141> CURRENT FILING DATE: 2001-08-31
 12 <160> NUMBER OF SEQ ID NOS: 15
 14 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 1643
 18 <212> TYPE: DNA
 19 <213> ORGANISM: avian reovirus strain 176
 21 <221> NAME/KEY: CDS
 22 <222> LOCATION: (25)...(318)
 23 <223> OTHER INFORMATION: nucleotide sequence encoding P11 protein (SEQ ID
 26 <220> FEATURE:
 27 <221> NAME/KEY: misc_feature
 28 <222> LOCATION: (293)...(730)
 29 <223> OTHER INFORMATION: CDS encoding P16 protein (SEQ ID
 30 NO:3)
 32 <220> FEATURE:
 33 <221> NAME/KEY: misc_feature
 34 <222> LOCATION: (630)...(1607)
 35 <223> OTHER INFORMATION: CDS encoding sigma3 protein (SEQ
 36 ID NO:4)
 38 <400> SEQUENCE: 1
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 40 Met Leu Arg Met Pro Pro Gly Ser Cys
 41 1 5
 43 aac ggt gcg act gct gta ttt ggt aac gtt cat tgt cag gca gct caa 99
 44 Asn Gly Ala Thr Ala Val Phe Gly Asn Val His Cys Gln Ala Ala Gln
 45 10 15 20 25
 47 aac acg gca ggt ggt gat ttg caa gct acg tca tcc ata att gca tat 147
 48 Asn Thr Ala Gly Gly Asp Leu Gln Ala Thr Ser Ser Ile Ile Ala Tyr
 49 30 35 40
 51 tgg cct tat cta gcg gcg ggt ggt ttc tta tta att gtt atc att 195
 52 Trp Pro Tyr Leu Ala Ala Gly Gly Phe Leu Leu Ile Val Ile Ile
 53 45 50 55
 55 ttc gct ctt cta tac tgt tgt aag gct aag gtc aag gcg gac gct gca 243
 56 Phe Ala Leu Leu Tyr Cys Cys Lys Ala Lys Val Lys Ala Asp Ala Ala
 57 60 65 70
 59 cgt agt gtc ttc cat cgt gag ctg gta gcg ttg agt tct ggt aag cac 291
 60 Arg Ser Val Phe His Arg Glu Leu Val Ala Leu Ser Ser Gly Lys His
 61 75 80 85
 63 aat gca atg gct ccg cca tac gac gtt tgaagtgc aa cgatttaatt 338
 64 Asn Ala Met Ala Pro Pro Tyr Asp Val
 65 90 95
 67 tctgtccgct atcacttcgc gaacttgcta tcccatcatt tactgctata actggggctg 398

#2.
ENTERED

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68	acccatcaca	gtatttaac	attgagctcc	cacacactca	tcctctctat	tccaaattgc	458
69	ctactctgtt	atctcaacct	tgttagggtcc	acgtcggtc	gattcgccgg	ttcgctctct	518
70	attcaacatt	gtcaagtatt	tgtgagtacg	atttgctct	actattctcc	ccacacgcta	578
71	tcgttccatt	gcctgcattcc	gatcgccgtt	cttgcattat	agttcatgg	gatggcggtt	638
72	ctcaatccat	cgcagcgaag	agagggtcg	agcttgatac	tgtcattgac	ttcgaacgtg	698
73	actataagtc	atggcgattt	gacgccgatc	tatgaacggc	tgaccaatct	agaagcgtct	758
74	acggagttat	tacatcgctc	catttccgat	atattccacta	ctgtctcaaa	tatttctgca	818
75	aatttacaag	acatgaccca	taccttggat	gatgtaactg	ctaatttaga	cgggttgagg	878
76	accactgtta	ctgcacttca	ggattccgtc	tccattctgt	ctacaaaatgt	gactgactta	938
77	acgaacacat	cctctgcgca	cgcggcgaca	ctatcttcac	ttcaaactac	ggttgacgga	998
78	aactccactg	ccatctccaa	tttgaagagt	gatgtatcgt	cgaacgggtt	agctattaca	1058
79	gatctgcagg	atcggtttaa	atcattggag	tctaccgcga	gtcatggct	atcttttcg	1118
80	cctccgcetta	gtgtcgctga	cggcggtt	tcattagaca	tggaccccta	cttctgttct	1178
81	caacgagttt	ctttaacatc	atactcgccg	gaggctcaac	taatgcaatt	tcggtggatg	1238
82	gcacggggtt	ctaacggatc	atctgatacc	attgacatga	ccgtaaacgc	tcactgtcat	1298
83	ggaagacgca	ctgatttat	atggtcg	acggaaatc	tcacggtcac	tagtaacgtc	1358
84	gtgttattaa	ccttcgattt	aagtgcatac	acgcataatcc	catcagacact	agcacgtctt	1418
85	gttcccagtg	cgggattcca	agctgcgtcg	ttccctgtgg	acgtatcatt	caccgcgat	1478
86	tctgcgactc	atgcgtacca	agcgtatggg	gtgtactcga	gctcacgtgt	cttcacaatt	1538
87	acttcccaa	ccggaggtga	tggtacagcg	aacattcg	ccttgaccgt	gcgtaccggc	1598
88	atcgacac	aagggtgtggc	gccgtactgg	gattggttat	tcatc		1643

90 <210> SEQ ID NO: 2

91 <211> LENGTH: 98

92 <212> TYPE: PRT

93 <213> ORGANISM: avian reovirus strain 176

95 <400> SEQUENCE: 2

96	Met	Leu	Arg	Met	Pro	Pro	Gly	Ser	Cys	Asn	Gly	Ala	Thr	Ala	Val	Phe
97	1			5					10						15	
98	Gly	Asn	Val	His	Cys	Gln	Ala	Ala	Gln	Asn	Thr	Ala	Gly	Gly	Asp	Leu
99					20				25						30	
100	Gln	Ala	Thr	Ser	Ser	Ile	Ile	Ala	Tyr	Trp	Pro	Tyr	Leu	Ala	Ala	Gly
101						35			40						45	
102	Gly	Gly	Phe	Leu	Leu	Ile	Val	Ile	Ile	Phe	Ala	Leu	Leu	Tyr	Cys	Cys
103						50			55						60	
104	Lys	Ala	Lys	Val	Lys	Ala	Asp	Ala	Ala	Arg	Ser	Val	Phe	His	Arg	Glu
105						65			70						75	80
106	Leu	Val	Ala	Leu	Ser	Ser	Gly	Lys	His	Asn	Ala	Met	Ala	Pro	Pro	Tyr
107						85				90					95	

108 Asp Val

110 <210> SEQ ID NO: 3

111 <211> LENGTH: 146

112 <212> TYPE: PRT

113 <213> ORGANISM: avian reovirus strain 176

115 <400> SEQUENCE: 3

116	Met	Gln	Trp	Leu	Arg	His	Thr	Thr	Phe	Glu	Val	Gln	Arg	Phe	Asn	Phe
117	1			5					10						15	
118	Cys	Pro	Leu	Ser	Leu	Arg	Glu	Leu	Ala	Ile	Pro	Ser	Phe	Thr	Ala	Ile
119					20				25						30	
120	Thr	Gly	Ala	Asp	Pro	Ser	Gln	Tyr	Phe	Asn	Ile	Glu	Leu	Pro	His	Thr

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```

121      35          40          45
122 His Pro Leu Tyr Ser Lys Leu Pro Thr Leu Leu Ser Gln Pro Cys Arg
123      50          55          60
124 Val His Val Arg Leu Ile Arg Arg Phe Ala Leu Tyr Ser Thr Leu Ser
125      65          70          75          80
126 Ser Ile Cys Glu Tyr Asp Cys Ala Leu Leu Phe Ser Pro His Ala Ile
127      85          90          95
128 Val Pro Leu Pro Ala Ser Asp Arg Arg Ser Cys Leu Ile Val His Trp
129      100         105         110
130 Asp Gly Gly Ser Gln Ser Ile Ala Ala Lys Arg Gly Arg Gln Leu Asp
131      115         120         125
132 Thr Val Ile Asp Phe Glu Arg Asp Tyr Lys Ser Trp Arg Phe Asp Ala
133      130         135         140
134 Asp Leu
135 145
137 <210> SEQ ID NO: 4
138 <211> LENGTH: 326
139 <212> TYPE: PRT
140 <213> ORGANISM: avian reovirus strain 176
142 <400> SEQUENCE: 4
143 Met Ala Gly Leu Asn Pro Ser Gln Arg Arg Glu Val Val Ser Leu Ile
144      1           5           10          15
145 Leu Ser Leu Thr Ser Asn Val Thr Ile Ser His Gly Asp Leu Thr Pro
146      20          25          30
147 Ile Tyr Glu Arg Leu Thr Asn Leu Glu Ala Ser Thr Glu Leu Leu His
148      35          40          45
149 Arg Ser Ile Ser Asp Ile Ser Thr Thr Val Ser Asn Ile Ser Ala Asn
150      50          55          60
151 Leu Gln Asp Met Thr His Thr Leu Asp Asp Val Thr Ala Asn Leu Asp
152      65          70          75          80
153 Gly Leu Arg Thr Thr Val Thr Ala Leu Gln Asp Ser Val Ser Ile Leu
154      85          90          95
155 Ser Thr Asn Val Thr Asp Leu Thr Asn Thr Ser Ser Ala His Ala Ala
156      100         105         110
157 Thr Leu Ser Ser Leu Gln Thr Thr Val Asp Gly Asn Ser Thr Ala Ile
158      115         120         125
159 Ser Asn Leu Lys Ser Asp Val Ser Ser Asn Gly Leu Ala Ile Thr Asp
160      130         135         140
161 Leu Gln Asp Arg Val Lys Ser Leu Glu Ser Thr Ala Ser His Gly Leu
162      145         150         155          160
163 Ser Phe Ser Pro Pro Leu Ser Val Ala Asp Gly Val Val Ser Leu Asp
164      165         170         175
165 Met Asp Pro Tyr Phe Cys Ser Gln Arg Val Ser Leu Thr Ser Tyr Ser
166      180         185         190
167 Ala Glu Ala Gln Leu Met Gln Phe Arg Trp Met Ala Arg Gly Thr Asn
168      195         200         205
169 Gly Ser Ser Asp Thr Ile Asp Met Thr Val Asn Ala His Cys His Gly
170      210         215         220
171 Arg Arg Thr Asp Tyr Met Met Ser Ser Thr Gly Asn Leu Thr Val Thr

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Input Set : A:\78973-1C seq 28-08-01 v1.txt
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172	225	230	235	240
173	Ser Asn Val Val Leu Leu Thr Phe Asp Leu Ser Asp Ile Thr His Ile			
174	245	250	255	
175	Pro Ser Asp Leu Ala Arg Leu Val Pro Ser Ala Gly Phe Gln Ala Ala			
176	260	265	270	
177	Ser Phe Pro Val Asp Val Ser Phe Thr Arg Asp Ser Ala Thr His Ala			
178	275	280	285	
179	Tyr Gln Ala Tyr Gly Val Tyr Ser Ser Ser Arg Val Phe Thr Ile Thr			
180	290	295	300	
181	Phe Pro Thr Gly Gly Asp Gly Thr Ala Asn Ile Arg Ser Leu Thr Val			
182	305	310	315	320
183	Arg Thr Gly Ile Asp Thr			
184	325			
186	<210> SEQ ID NO: 5			
187	<211> LENGTH: 1643			
188	<212> TYPE: DNA			
189	<213> ORGANISM: avian reovirus strain 138			
191	<220> FEATURE:			
192	<221> NAME/KEY: CDS			
193	<222> LOCATION: (25)...(318)			
194	<223> OTHER INFORMATION: nucleotide sequence encoding P11 protein (SEQ ID NO:6)			
196	<220> FEATURE:			
197	<221> NAME/KEY: misc_feature			
198	<222> LOCATION: (293)...(730)			
199	<223> OTHER INFORMATION: CDS encoding P16 protein (SEQ ID NO:7)			
201	<220> FEATURE:			
202	<221> NAME/KEY: misc_feature			
203	<222> LOCATION: (630)...(1607)			
204	<223> OTHER INFORMATION: CDS encoding sigma3 protein (SEQ ID NO:8)			
206	<400> SEQUENCE: 5			
207	gcttttcaa tcccttgttt gtcg atg ctg cgt atg cct ccc ggt tcg tgt			51
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209	1 5			
211	aac ggt gca aca gct atc ttt ggt aac gtc cat tgt cag gcg gct caa			99
212	Asn Gly Ala Thr Ala Ile Phe Gly Asn Val His Cys Gln Ala Ala Gln			
213	10 15 20 25			
215	aat act gcc ggc ggc gac ttg caa gct acc tca tcc ata att gcc tat			147
216	Asn Thr Ala Gly Gly Asp Leu Gln Ala Thr Ser Ser Ile Ile Ala Tyr			
217	30 35 40			
219	tgg cct tat cta gcg gcg ggt ggt ttt ttg ttg att att att			195
220	Trp Pro Tyr Leu Ala Ala Gly Gly Phe Leu Leu Ile Ile Ile Ile			
221	45 50 55			
223	ttt gcc atc ttc tac tgt tgt aag gct aaa gtt aaa gcg gac gct gca			243
224	Phe Ala Ile Phe Tyr Cys Cys Lys Ala Lys Val Lys Ala Asp Ala Ala			
225	60 65 70			
227	cgg agt gtt ttc cac cgt gag ctt gta gca ctg agc tct ggt aag cac			291
228	Arg Ser Val Phe His Arg Glu Leu Val Ala Leu Ser Ser Gly Lys His			
229	75 80 85			
231	aat gca atg gct ccg cca tac gac gtt tgaagtgc当地 cgctttgatt			338

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Input Set : A:\78973-1C seq 28-08-01 v1.txt
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232	Asn Ala Met Ala Pro Pro Tyr Asp Val		
233	90	95	
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236	acccatcacg ttatTTTaaT attgagctt cgacacgcA tcctctac tctaaggTgc	458	
237	cgactctgtt atcgcagccc tgccgagtt acgtgcgtt gattcgtaga ttgcgtct	518	
238	gttcaacgct gtcgagtatc tgcgagtacg attgtgcgtt actacttcc ccacacgcca	578	
239	tcactccact gtcctcatcc gatcagcgat ctatcttat agttcattgg gatggcgggt	638	
240	ctcaatccat cacagcgaag agaggtcgTC agcttgatac tgcattgac ttgaacgcg	698	
241	catataaATC atggcgattt gacgccaATC tatgaacggT tgaccagTT agaagcgTCT	758	
242	gcggaaatCAC tatATCGCTC cATTCCAGC atgtctacta ccgtttcaga catttcagca	818	
243	gatttgcaga acgtgactcg cgcTTggat gatgtgactg ctaatttaga tggtatgaga	878	
244	gtcaccatttA ctacgcttca agattctgtg tccactctt caacgactgt aactgatttA	938	
245	acaAAACACt cttctgtca ctggaaAgca ctgtcttac tccgaactat agttgatggg	998	
246	aactccacta ccattgataa ttgaaaAGt gatgtatcat caaacggTct tgctatcaca	1058	
247	gacctgcaga gtcgtgttaa atccttgaa tctgtttcga gtcacgggt atcttttgc	1118	
248	cctccttta gtgtcgctga cgacgtatg tcgttgatg tggaccctt ctTTGCTCT	1178	
249	cagcgagtc ctttgacatc atactcagca gaagctcaac tgatgcaatt ccaatggatg	1238	
250	gcaagaggTg ctaacggatc atcagacact attgacatga ccgtcaatgc tcactgtcat	1298	
251	gggagacgca ctgattacat aatgtcgTcc acgggaggTc ttacagttac tagtaatgCc	1358	
252	gtgtctttaa cttcgactt gagttacatt acacgcctt caccagacct ctgcgtctt	1418	
253	gttcccagtg caggattcca agccggtcg ttccccgtgg atgtatcctt caccagagat	1478	
254	tcgacaactc atacatatca agcttatgga gtgtattcta gttcggtgtt attaccatc	1538	
255	actttcccgA ctgggtgtga cggTcccga aatatccgtt tcctaaccgt gcttaccggc	1598	
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259	<211> LENGTH: 98		
260	<212> TYPE: PRT		
261	<213> ORGANISM: avian reovirus strain 138		
263	<400> SEQUENCE: 6		
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265	1 5 10 15		
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267	20 25 30		
268	Gln Ala Thr Ser Ser Ile Ile Ala Tyr Trp Pro Tyr Leu Ala Ala Gly		
269	35 40 45		
270	Gly Gly Phe Leu Leu Ile Ile Ile Ile Phe Ala Ile Phe Tyr Cys Cys		
271	50 55 60		
272	Lys Ala Lys Val Lys Ala Asp Ala Ala Arg Ser Val Phe His Arg Glu		
273	65 70 75 80		
274	Leu Val Ala Leu Ser Ser Gly Lys His Asn Ala Met Ala Pro Pro Tyr		
275	85 90 95		
276	Asp Val		
278	<210> SEQ ID NO: 7		
279	<211> LENGTH: 146		
280	<212> TYPE: PRT		
281	<213> ORGANISM: avian reovirus strain 138		
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285	1 5 10 15		

VERIFICATION SUMMARY
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L:9 M:270 C: Current Application Number differs, Replaced Current Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date